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## RAW SEQUENCE LISTING

DATE: 09/21/2001

PATENT APPLICATION: US/09/944,849

TIME: 18:10:39

Input Set : A:\ES.txt

Output Set: N:\CRF3\09212001\I944849.raw

#2

P.5

ENTERED

```

3 <110> APPLICANT: Nickoloff, Brian
4 Miele, Lucio
6 <120> TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND
TREATMENT OF
7 MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH PATHWAY
9 <130> FILE REFERENCE: 212583
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/944,849
12 <141> CURRENT FILING DATE: 2001-08-31
14 <150> PRIOR APPLICATION NUMBER: US 60/229,614
15 <151> PRIOR FILING DATE: 2000-08-31
17 <160> NUMBER OF SEQ ID NOS: 18
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 7332
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Constitutively Active Notch-1
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(7332)
32 <223> OTHER INFORMATION:
35 <220> FEATURE:
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (5288)..(5288)
38 <223> OTHER INFORMATION: n is "a," "t," "g," or "c"
41 <220> FEATURE:
42 <221> NAME/KEY: misc_feature
43 <222> LOCATION: (5359)..(5359)
44 <223> OTHER INFORMATION: n is "a," "t," "g," or "c"
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48 atg ccg ccg ctc ctg gcg ccc ctg ctc tgc ctg gcg ctg ctg ccc gcg 48
49 Met Pro Pro Leu Leu Ala Pro Leu Leu Cys Leu Ala Leu Leu Pro Ala
50 1 5 10 15
52 ctc gcc gca cga ggc ccg cga tgc tcc cag ccc ggt gag acc tgc ctg 96
53 Leu Ala Ala Arg Gly Pro Arg Cys Ser Gln Pro Gly Glu Thr Cys Leu
54 20 25 30
56 aat ggc ggg aag tgt gaa gcg gcc aat ggc acg gag gcc tgc gtc tgt 144
57 Asn Gly Gly Lys Cys Glu Ala Ala Asn Gly Thr Glu Ala Cys Val Cys
58 35 40 45
60 ggc ggg gcc ttc gtg ggc ccg cga tgc cag gac ccc aac ccg tgc ctc 192
61 Gly Gly Ala Phe Val Gly Pro Arg Cys Gln Asp Pro Asn Pro Cys Leu
62 50 55 60
64 agc acc ccc tgc aag aac gcc ggg aca tgc cac gtg gtg gac cgc aga 240
65 Ser Thr Pro Cys Lys Asn Ala Gly Thr Cys His Val Val Asp Arg Arg
66 65 70 75 80
68 ggc gtg gca gac tat gcc tgc agc tgt gcc ctg ggc ttc tct ggg ccc 288
69 Gly Val Ala Asp Tyr Ala Cys Ser Cys Ala Leu Gly Phe Ser Gly Pro

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70	85	90	95	
72	ctc tgc ctg aca ccc ctg gac aac gcc tgc ctc acc aac ccc tgc cgc	336		
73	Leu Cys Leu Thr Pro Leu Asp Asn Ala Cys Leu Thr Asn Pro Cys Arg			
74	100 105 110			
76	aac ggg ggc acc tgc gac ctg ctc acg ctg acg gag tac aag tgc cgc	384		
77	Asn Gly Gly Thr Cys Asp Leu Leu Thr Leu Thr Glu Tyr Lys Cys Arg			
78	115 120 125			
80	tgc ccg ccc ggc tgg tca ggg aaa tcg tgc cag cag gct gac ccg tgc	432		
81	Cys Pro Pro Gly Trp Ser Gly Lys Ser Cys Gln Gln Ala Asp Pro Cys			
82	130 135 140			
84	gcc tcc aac ccc tgc gcc aac ggt ggc cag tgc ctg ccc ttc gag gcc	480		
85	Ala Ser Asn Pro Cys Ala Asn Gly Gly Gln Cys Leu Pro Phe Glu Ala			
86	145 150 155 160			
88	tcc tac atc tgc cac tgc cca ccc agc ttc cat ggc ccc acc tgc cgg	528		
89	Ser Tyr Ile Cys His Cys Pro Pro Ser Phe His Gly Pro Thr Cys Arg			
90	165 170 175			
92	cag gat gtc aac gag tgt ggc cag aag ccc agg ctt tgc cgc cac gga	576		
93	Gln Asp Val Asn Glu Cys Gly Gln Lys Pro Arg Leu Cys Arg His Gly			
94	180 185 190			
96	ggc acc tgc cac aac gag gtc ggc tcc tac cgc tgc gtc tgc cgc gcc	624		
97	Gly Thr Cys His Asn Glu Val Gly Ser Tyr Arg Cys Val Cys Arg Ala			
98	195 200 205			
100	acc cac act ggc ccc aac tgc gag cgg ccc tac gtg ccc tgc agc ccc	672		
101	Thr His Thr Gly Pro Asn Cys Glu Arg Pro Tyr Val Pro Cys Ser Pro			
102	210 215 220			
104	tcg ccc tgc cag aac ggg ggc acc tgc cgc ccc acg ggc gac gtc acc	720		
105	Ser Pro Cys Gln Asn Gly Gly Thr Cys Arg Pro Thr Gly Asp Val Thr			
106	225 230 235 240			
108	cac gag tgt gcc tgc ctg cca ggc ttc acc ggc cag aac tgt gag gaa	768		
109	His Glu Cys Ala Cys Leu Pro Gly Phe Thr Gly Gln Asn Cys Glu Glu			
110	245 250 255			
112	aat atc gac gat tgt cca gga aac aac tgc aag aac ggg ggt gcc tgt	816		
113	Asn Ile Asp Asp Cys Pro Gly Asn Asn Cys Lys Asn Gly Gly Ala Cys			
114	260 265 270			
116	gtg gac ggc gtg aac acc tac aac tgc ccg tgc ccg cca gag tgg aca	864		
117	Val Asp Gly Val Asn Thr Tyr Asn Cys Pro Cys Pro Pro Glu Trp Thr			
118	275 280 285			
120	ggt cag tac tgt acc gag gat gtg gac gag tgc cag ctg atg cca aat	912		
121	Gly Gln Tyr Cys Thr Glu Asp Val Asp Glu Cys Gln Leu Met Pro Asn			
122	290 295 300			
124	gcc tgc cag aac ggc ggg acc tgc cac aac acc cac ggt ggc tac aac	960		
125	Ala Cys Gln Asn Gly Gly Thr Cys His Asn Thr His Gly Gly Tyr Asn			
126	305 310 315 320			
128	tgc gtg tgt gtc aac ggc tgg act ggt gag gac tgc agc gag aac att	1008		
129	Cys Val Cys Val Asn Gly Trp Thr Gly Glu Asp Cys Ser Glu Asn Ile			
130	325 330 335			
132	gat gac tgt gcc agc gcc gcc tgc ttc cac ggc gcc acc tgc cat gac	1056		
133	Asp Asp Cys Ala Ser Ala Ala Cys Phe His Gly Ala Thr Cys His Asp			
134	340 345 350			

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136 cgt gtg gcc tcc ttt tac tgc gag tgt ccc cat ggc cgc aca ggt ctg      1104
137 Arg Val Ala Ser Phe Tyr Cys Glu Cys Pro His Gly Arg Thr Gly Leu
138          355          360          365
140 ctg tgc cac ctc aac gac gca tgc atc agc aac ccc tgt aac gag ggc      1152
141 Leu Cys His Leu Asn Asp Ala Cys Ile Ser Asn Pro Cys Asn Glu Gly
142      370          375          380
144 tcc aac tgc gac acc aac cct gtc aat ggc aag gcc atc tgc acc tgc      1200
145 Ser Asn Cys Asp Thr Asn Pro Val Asn Gly Lys Ala Ile Cys Thr Cys
146 385          390          395          400
148 ccc tcg ggg tac acg ggc ccg gcc tgc agc cag gac gtg gat gag tgc      1248
149 Pro Ser Gly Tyr Thr Gly Pro Ala Cys Ser Gln Asp Val Asp Glu Cys
150          405          410          415
152 tcg ctg ggt gcc aac ccc tgc gag cat gcg ggc aag tgc atc aac acg      1296
153 Ser Leu Gly Ala Asn Pro Cys Glu His Ala Gly Lys Cys Ile Asn Thr
154          420          425          430
156 ctg ggc tcc ttc gag tgc cag tgt ctg cag ggc tac acg ggc ccc cga      1344
157 Leu Gly Ser Phe Glu Cys Gln Cys Leu Gln Gly Tyr Thr Gly Pro Arg
158      435          440          445
160 tgc gag atc gac gtc aac gag tgc gtc tcg aac ccg tgc cag aac gac      1392
161 Cys Glu Ile Asp Val Asn Glu Cys Val Ser Asn Pro Cys Gln Asn Asp
162      450          455          460
164 gcc acc tgc ctg gac cag att ggg gag ttc cag tgc atg tgc atg ccc      1440
165 Ala Thr Cys Leu Asp Gln Ile Gly Glu Phe Gln Cys Met Cys Met Pro
166 465          470          475          480
168 ggc tac gag ggt gtg cac tgc gag gtc aac aca gac gag tgt gcc agc      1488
169 Gly Tyr Glu Gly Val His Cys Glu Val Asn Thr Asp Glu Cys Ala Ser
170          485          490          495
172 agc ccc tgc ctg cac aat ggc cgc tgc ctg gac aag atc aat gag ttc      1536
173 Ser Pro Cys Leu His Asn Gly Arg Cys Leu Asp Lys Ile Asn Glu Phe
174          500          505          510
176 cag tgc gag tgc ccc acg ggc ttc act ggg cat ctg tgc cag tac gat      1584
177 Gln Cys Glu Cys Pro Thr Gly Phe Thr Gly His Leu Cys Gln Tyr Asp
178      515          520          525
180 gtg gac gag tgt gcc agc acc ccc tgc aag aat ggt gcc aag tgc ctg      1632
181 Val Asp Glu Cys Ala Ser Thr Pro Cys Lys Asn Gly Ala Lys Cys Leu
182      530          535          540
184 gac gga ccc aac act tac acc tgt gtg tgc acg gaa ggg tac acg ggg      1680
185 Asp Gly Pro Asn Thr Tyr Thr Cys Val Cys Thr Glu Gly Tyr Thr Gly
186 545          550          555          560
188 acg cac tgc gag gtg gac atc gat gag tgc gac ccc gac ccc tgc cac      1728
189 Thr His Cys Glu Val Asp Ile Asp Glu Cys Asp Pro Asp Pro Cys His
190          565          570          575
192 tac ggc tcc tgc aag gac ggc gtc gcc acc ttc acc tgc ctc tgc cgc      1776
193 Tyr Gly Ser Cys Lys Asp Gly Val Ala Thr Phe Thr Cys Leu Cys Arg
194          580          585          590
196 cca ggc tac acg ggc cac cac tgc gag acc aac atc aac gag tgc tcc      1824
197 Pro Gly Tyr Thr Gly His His Cys Glu Thr Asn Ile Asn Glu Cys Ser
198      595          600          605
200 agc cag ccc tgc cgc cta cgg ggc acc tgc cag gac ccg gac aac gcc      1872

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201	Ser	Gln	Pro	Cys	Arg	Leu	Arg	Gly	Thr	Cys	Gln	Asp	Pro	Asp	Asn	Ala	
202		610					615				620						
204	tac	ctc	tgc	ttc	tgc	ctg	aag	ggg	acc	aca	gga	ccc	aac	tgc	gag	atc	1920
205	Tyr	Leu	Cys	Phe	Cys	Leu	Lys	Gly	Thr	Thr	Gly	Pro	Asn	Cys	Glu	Ile	
206	625					630					635					640	
208	aac	ctg	gat	gac	tgt	gcc	agc	agc	ccc	tgc	gac	tcg	ggc	acc	tgt	ctg	1968
209	Asn	Leu	Asp	Asp	Cys	Ala	Ser	Ser	Pro	Cys	Asp	Ser	Gly	Thr	Cys	Leu	
210					645					650						655	
212	gac	aag	atc	gat	ggc	tac	gag	tgt	gcc	tgt	gag	ccg	ggc	tac	aca	ggg	2016
213	Asp	Lys	Ile	Asp	Gly	Tyr	Glu	Cys	Ala	Cys	Glu	Pro	Gly	Tyr	Thr	Gly	
214				660					665					670			
216	agc	atg	tgt	aac	agc	aac	atc	gat	gag	tgt	gcg	ggc	aac	ccc	tgc	cac	2064
217	Ser	Met	Cys	Asn	Ser	Asn	Ile	Asp	Glu	Cys	Ala	Gly	Asn	Pro	Cys	His	
218			675					680					685				
220	aac	ggg	ggc	acc	tgc	gag	gac	ggc	atc	aat	ggc	ttc	acc	tgc	cgc	tgc	2112
221	Asn	Gly	Gly	Thr	Cys	Glu	Asp	Gly	Ile	Asn	Gly	Phe	Thr	Cys	Arg	Cys	
222		690					695					700					
224	ccc	gag	ggc	tac	cac	gac	ccc	acc	tgc	ctg	tct	gag	gtc	aat	gag	tgc	2160
225	Pro	Glu	Gly	Tyr	His	Asp	Pro	Thr	Cys	Leu	Ser	Glu	Val	Asn	Glu	Cys	
226	705					710					715					720	
228	aac	agc	aac	ccc	tgc	gtc	cac	ggg	gcc	tgc	cgg	gac	agc	ctc	aac	ggg	2208
229	Asn	Ser	Asn	Pro	Cys	Val	His	Gly	Ala	Cys	Arg	Asp	Ser	Leu	Asn	Gly	
230				725						730						735	
232	tac	aag	tgc	gac	tgt	gac	cct	ggg	tgg	agt	ggg	acc	aac	tgt	gac	atc	2256
233	Tyr	Lys	Cys	Asp	Cys	Asp	Pro	Gly	Trp	Ser	Gly	Thr	Asn	Cys	Asp	Ile	
234				740					745					750			
236	aac	aac	aac	gag	tgt	gaa	tcc	aac	cct	tgt	gtc	aac	ggc	ggc	acc	tgc	2304
237	Asn	Asn	Asn	Glu	Cys	Glu	Ser	Asn	Pro	Cys	Val	Asn	Gly	Gly	Thr	Cys	
238			755					760					765				
240	aaa	gac	atg	acc	agt	ggc	atc	gtg	tgc	acc	tgc	cgg	gag	ggc	ttc	agc	2352
241	Lys	Asp	Met	Thr	Ser	Gly	Ile	Val	Cys	Thr	Cys	Arg	Glu	Gly	Phe	Ser	
242		770				775					780						
244	ggt	ccc	aac	tgc	cag	acc	aac	atc	aac	gag	tgt	gcg	tcc	aac	cca	tgt	2400
245	Gly	Pro	Asn	Cys	Gln	Thr	Asn	Ile	Asn	Glu	Cys	Ala	Ser	Asn	Pro	Cys	
246	785					790					795					800	
248	ctg	aac	aag	ggc	acg	tgt	att	gac	gac	gtt	gcc	ggg	tac	aag	tgc	aac	2448
249	Leu	Asn	Lys	Gly	Thr	Cys	Ile	Asp	Asp	Val	Ala	Gly	Tyr	Lys	Cys	Asn	
250					805					810						815	
252	tgc	ctg	ctg	ccc	tac	aca	ggt	gcc	acg	tgt	gag	gtg	gtg	ctg	gcc	ccg	2496
253	Cys	Leu	Leu	Pro	Tyr	Thr	Gly	Ala	Thr	Cys	Glu	Val	Val	Leu	Ala	Pro	
254				820					825					830			
256	tgt	gcc	ccc	agc	ccc	tgc	aga	aac	ggc	ggg	gag	tgc	agg	caa	tcc	gag	2544
257	Cys	Ala	Pro	Ser	Pro	Cys	Arg	Asn	Gly	Gly	Glu	Cys	Arg	Gln	Ser	Glu	
258			835					840					845				
260	gac	tat	gag	agc	ttc	tcc	tgt	gtc	tgc	ccc	acg	gct	ggg	gcc	aaa	ggg	2592
261	Asp	Tyr	Glu	Ser	Phe	Ser	Cys	Val	Cys	Pro	Thr	Ala	Gly	Ala	Lys	Gly	
262		850					855					860					
264	cag	acc	tgt	gag	gtc	gac	atc	aac	gag	tgc	gtt	ctg	agc	ccg	tgc	cgg	2640
265	Gln	Thr	Cys	Glu	Val	Asp	Ile	Asn	Glu	Cys	Val	Leu	Ser	Pro	Cys	Arg	

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```

266 865      870      875      880
268 cac ggc gca tcc tgc cag aac acc cac ggc gss tac cgc tgc cac tgc      2688
W--> 269 His Gly Ala Ser Cys Gln Asn Thr His Gly Xaa Tyr Arg Cys His Cys
270      885      890      895
272 cag gcc ggc tac agt ggg cgc aac tgc gag acc gac atc gac gac tgc      2736
273 Gln Ala Gly Tyr Ser Gly Arg Asn Cys Glu Thr Asp Ile Asp Asp Cys
274      900      905      910
276 cgg ccc aac ccg tgt cac aac ggg ggc tcc tgc aca gac ggc atc aac      2784
277 Arg Pro Asn Pro Cys His Asn Gly Gly Ser Cys Thr Asp Gly Ile Asn
278      915      920      925
280 acg gcc ttc tgc gac tgc ctg ccc ggc ttc cgg ggc act ttc tgt gag      2832
281 Thr Ala Phe Cys Asp Cys Leu Pro Gly Phe Arg Gly Thr Phe Cys Glu
282      930      935      940
284 gag gac atc aac gag tgt gcc agt gac ccc tgc cgc aac ggg gcc aac      2880
285 Glu Asp Ile Asn Glu Cys Ala Ser Asp Pro Cys Arg Asn Gly Ala Asn
286      945      950      955      960
288 tgc acg gac tgc gtg gac agc tac acg tgc acc tgc ccc gca ggc ttc      2928
289 Cys Thr Asp Cys Val Asp Ser Tyr Thr Cys Thr Cys Pro Ala Gly Phe
290      965      970      975
292 agc ggg atc cac tgt gag aac aac acg cct gac tgc aca gag agc tcc      2976
293 Ser Gly Ile His Cys Glu Asn Asn Thr Pro Asp Cys Thr Glu Ser Ser
294      980      985      990
296 tgc ttc aac ggt ggc acc tgc gtg gac ggc atc aac tcg ttc acc tgc      3024
297 Cys Phe Asn Gly Gly Thr Cys Val Asp Gly Ile Asn Ser Phe Thr Cys
298      995      1000      1005
300 ctg tgt cca ccc ggc ttc acg ggc agc tac tgc cag cac gta gtc      3069
301 Leu Cys Pro Pro Gly Phe Thr Gly Ser Tyr Cys Gln His Val Val
302      1010      1015      1020
304 aat gag tgc gac tca cga ccc tgc ctg cta ggc ggc acc tgt cag      3114
305 Asn Glu Cys Asp Ser Arg Pro Cys Leu Leu Gly Gly Thr Cys Gln
306      1025      1030      1035
308 gac ggt cgc ggt ctc cac agg tgc acc tgc ccc cag ggc tac act      3159
309 Asp Gly Arg Gly Leu His Arg Cys Thr Cys Pro Gln Gly Tyr Thr
310      1040      1045      1050
312 ggc ccc aac tgc cag aac ctt gtg cac tgg tgt gac tcc tcg ccc      3204
313 Gly Pro Asn Cys Gln Asn Leu Val His Trp Cys Asp Ser Ser Pro
314      1055      1060      1065
316 tgc aag aac ggc ggc aaa tgc tgg cag acc cac acc cag tac cgc      3249
317 Cys Lys Asn Gly Gly Lys Cys Trp Gln Thr His Thr Gln Tyr Arg
318      1070      1075      1080
320 tgc gag tgc ccc agc ggc tgg acc ggc ctt tac tgc gac gtg ccc      3294
321 Cys Glu Cys Pro Ser Gly Trp Thr Gly Leu Tyr Cys Asp Val Pro
322      1085      1090      1095
324 agc gtg tcc tgt gag gtg gct gcg cag cga caa ggt gtt gac gtt      3339
325 Ser Val Ser Cys Glu Val Ala Ala Gln Arg Gln Gly Val Asp Val
326      1100      1105      1110
328 gcc cgc ctg tgc cag cat gga ggg ctc tgt gtg gac gcg ggc aac      3384
329 Ala Arg Leu Cys Gln His Gly Gly Leu Cys Val Asp Ala Gly Asn
330      1115      1120      1125

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Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/944,849

DATE: 09/21/2001

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Input Set : A:\ES.txt

Output Set: N:\CRF3\09212001\I944849.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:501 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:505 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:1162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:1166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:2598 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:2618 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11  
L:2638 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12  
L:2658 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13  
L:2678 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14  
L:2692 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15  
L:2740 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16  
L:2743 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
L:2749 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
L:2755 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
L:2789 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17  
L:2826 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18  
L:2829 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18